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mo60904.r AU136010

cn27902.x dd89910.y dad73b08. dad68h09.

v128906.r MR4-HT105

AU139958

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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW951855 654 bp mRNA EST 01-JUN-2000
EST363925 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
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Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Genomic Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
              AZ267276 AAG19096 AAG59563 AAG19096 BI183393 AAG1917523 AAG19177 AAW619117 AAW619117 AAG136010 BG886115 AG597346 AAG50106 BG997346 AAG50106 AG60739301 AG597346 AAG50106 AG60739134 AW050106 AG59734 AAG50106 AG60739124 AAG50106 AG60739124 AAG50106 AG60739124 AAG50106 AG60739124 AAG50106 AG60739124 AAG50106 AG607323 AIRS29064 AAG50096 AAG500
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1. .654
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/clone_lib="MAGE resequences, MAGB"
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AZ939124
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AUTHORS
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AA554966 nh35c11.s
AA327423 uj22e09.y
AA229062 nc49907.r
T28396 EST41738 Hu
AM619116 436 MACC
AI785019 uj22e09.x
AA230070 nc49b06.s
AA659567 nc4306.s
AA659567 nc4306.s
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequencing Center information can be

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/note="Wector: paMP10; Site_1: Not1; Site_2: EcoRI; Ist strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5.000-10. ON microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
DNA Sequencing by: Washington University Genome: Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbbp/image/image.html Insert Length: 362 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 383.
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           DB 10;
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RESULT

M.D.

Euteleostomi;

Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

AA524966 568 bp mRNA EST 05-AUG-1997 nh35c11.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:954356 similar to 9b:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.

AA524966 AA524966.1 GI:2265894

ACCESSION VERSION KEYWORDS SOURCE

AA524966/c DEFINITION

LOCUS

human.

ORGANISM

Email: cgapbs-rémail.nih.gov Itssue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.I Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

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Contact: Robert Strausberg, Ph.D.

Tumor Gene Index Unpublished (1997)

JOURNAL

AUTHORS TITLE

REFERENCE

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135 TGTGGTATCCTGGTGGAGTTGTGAACAGAGTACCCTATCCCAGTCCCAATTGTGTCAAAA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Kidney; Vector: PME18S-FL3; Site_1: DraIII (CACCTGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an Oligo(dT) primer stranded cDNA was primed with an Oligo(dT) primer stranded cDNA was [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct braIII sites of the PME18S-FL3 vector (5' site CACCTGTGTG, 3' site CACCATGTG). KNOI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACCAAA."
                                                                                                                                                                                        Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 724)

Marai, Hillier L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Wasterston, R.

The Washu-HHMI Mouse EST Project
Unpublished (1996)

Contact: Marra M./Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810

Email: Mouseest@washon.wustledu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgtggtaccctggcggcatggtgagcagagtgccctatcccagtcccacttgtgtcaaaa 3436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTACACTCGGCCCCCTCAGGGGCTGACAAGCCAGGAGTGACTACTCTGCCTCCGAAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GCCTGGGCTGCGGCGGCAGC-GCAATGCCGCTATGGGGACTTGGGTAGTCAGCCCCTATG 74
A1317423 724 bp mRNA EST 17-DEC-1998 uj22e09.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAE:1920712 5' similar to qb:X33779 Mouse mRNA for androgen A1317423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 462.2; DB 10;
82.8%; Pred. No. 2.4e-49;
tive 0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: custom primer used
High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1920712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                     AI317423.1 GI:4032690
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                                                                                                                                                                              house mouse.
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Best Local
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                                                         DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                               ORGANISM
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AUTHORS
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                                                                                                                       ACCESSION
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KEYWORDS
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                    AI317423
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Email: cgapbs remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA bibrary Arrayed by: Genome Systems Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 388)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                 aagcagggatgactctggggagcccggaagctgaagaacttggtaatctgaaactacagg 3796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggaaggagagcttccagcaccaccaccactgaggagacacccagaagctgacag 3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3857 tgtcacacattgaaggc-tatgaatgtcagcccatcttt--ctgaatgtcctggaagcca 3913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA229063 388 bp mRNA EST 21-AUG-1997 nc49g07.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1011516 similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
3437 gcgaaatgggcccctggatggatagctactccggaccttacggggacatgcgtttggaga 3496
                                                                                                                                                                                                              255 GTACCAGGGACCATGTTTACCCATCACTATTACTTTCCACCCAGAAGACCTGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCACACATTGAAAGCTTTTGAATGTCAGCCTATCTTTTCTTAACGTCCCTGGAAGCCA
                                                                                                           Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-bio.llnI.gov/bbrp/image/image.html
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Fri

BASE COUNT ORIGIN

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//note="Vector: pamp10; Site_1: Not1; Site_2: EcoRI; Ist Strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAmp10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
    cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -20ml3 revl ET from Amersham
High quality sequence stop: 341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctctattgatgtacagtctgtcatgaacatgttcctgaattctatttgctgggctttttt 4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4980 gtgccagccacacaaacgtttacttatcttatgccacgggaagtttagagagctaagatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Score 369; DB 10;
Similarity 100.0%; Pred. No. 1.6e-37;
59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                          /clone="IMAGE:1011516"
/clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                       /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 369; Conservative
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                                                                          /note="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st Strand CDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cONA was ligated to ECORI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
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1 (bases 1 to 369)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 TCACTITTGACCTGCTAATCAAGTCACACGTGAGCGTGGACTTTCCGGAAATGATGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA229062 369 bp mRNA EST '21-AUG-1997 nc49907.rl NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:1011516 sinilar to 9b:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagagatcatctctgtgcaagtgcccaagatcctttctgggaaagtcaagcccatctatt
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                               Score 380.6; DB 10; Length 388;
Pred. No. 5.6e-39;
0; Mismatches 4; Indels 0;
                                       /dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr3"
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0°
Matches 383; Conservative
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human.

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

ACCESSION VERSION

AA229062/c LOCUS

DEFINITION

Fri Jan

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301 AAAATTCTTTGATGNACTTCGGATGNACTACA-CAAGGGACTCGGTCGTATCATTGCATG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                            Anim. Genet. 32 (2), 66-72 (2001)
21314990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GCAGCAGGAGACCAGTCCCCGGCGCGCA----
                                                                                                                                                                              AW619116 573 bp mRNA
436 MARC PBE Sus scrofa cDNA
AW619116 GI:7325300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: GGAAACAGCTATGACCATG BACKWARD: GTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Similarity 77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, Main.

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N., Kirkness, E.F., Welnstock, K.G., Gocayne, J.D., White,

O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayfon, R.A.,

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkledt, P.S., Kelley, J.M.,

Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Ferrich, A., Fischer, C., Hastings, G.A., He, W.-W.,

Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L.,

Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Weit,

Wolfer, Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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                                                                                                                                                                                                                                                                                                                                                                                                                   Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 277, 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.6e-36;
0; Mismatches 21;
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/db_xref="taxon:9606"
/clone_lib="Human Uterus"
/note="Organ: uterus"
108 c 92 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Best Local Similarity 94.5%;
Matches 381; Conservative
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        .C.E. and Keele,J.W.
Mapping of expressed sequence tags from a porcine early embryonic
cDNA library
                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad
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                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (285.8 1 to 573) Smith, T.P.L., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.
                                                                                                                                                                                                    5', mRNA sequence.
4407 caaaagaaaaaatcccacatcctgctcaagacgcttctaccag 4449
                          360 CAAAAGGAAAAATCCCACATTCTGUTTCAGACGGTTTTACCAG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9823"
/clone_lib="MARC PBE"
/tissue_type="Day 12 whole embryos"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
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Mis musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 637)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
'E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Schurk,R., Ritter
Waterston,R. and Wilson,R.
The MashUNCI Mouse EST Project 1999
                                                                              2222
                                                                                                                                                 2223 gccgcagtcggccctggagtgccacccgagagagagttgcgtcccagagcctggagccgc 2282
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                                                                                                                                                                                                                                                                                                        agctgccccatccacgttgtccctgctggccccactttccccggcttaagcagctgctc 2402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                       375
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IMAGE:1920712 3' similar to gb.x53779 Mouse mRNA for androgen
receptor (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine, 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                               376 TTCGGCCCCAGCAAGGGCTGCAACAGCAGCGTCCGTCGGACGAGGATGCTTC
                                                                                                                                                                                                                                                                                                                                                                         2103 gcagcaagagactagccccaggcagcagcagcagcagcaggagggtgaggatggttctcccca
                                                                                                                                                                     316 ACAGCAATCAGCCCTGAGTGCCACCCGGAGAGCGGCTGCACCCCAGAGCCGGAGCAGC
                                                                                                                                                                                                                                                                                                                                        436 AGCTGCCCCATCCACGCTGTCCCTGCTGGGCCCCACTTTCCCCGGGTTTAAGCAGCTGCTC
                                                                          agcccatcgtagaggccccacaggctacctggtcctggatgaggaacagcaaccttcaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other_ESTS: uj22e09.yl
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/clone_lib="Sugano mouse kidney mkia"
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High quality sequence stop: 518.
Location/Qualifiers
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sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTGGAGCACA." 1 others
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                                                                                                                                                                                                                                                                                                                                                                             4659 accccagctcatgccccctttcagatgtcttctgcctgt--tataactctgcactactcc 4716
                                                                                                                                                                                                                                                                                                                                                                                                                       4775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tttgaatggtgttgtatgcctttaaatctgtgatgatcctcatatggcccagtgtcaagt 4955
                                                                                                                                                                                                                                                                                                                                                                                        | || || AAACCCACCTTGTTCCAGATGTCTTCTGCCTGTTATATAACTCTGCACTACTTC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA230070 349 bp mRNA EST 21-AUG-1997 nc49b06.s1 NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:1011443 similar to 9b:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 TTTGATTTCTGTTGTATTTCTTTGAATCTGTGATGATCCTCTTGTGGCCCCAGTGTCAA-T 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                            230 CTCTTTCACCCTCCCATGGCACATTTTGAATCTGCTGCTATTGTGGCTCCTGCCTTTGT
                                                                                                                                                                                                23;
                                                                                                                                                                            Length 637
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                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5014 cacgggaagtttagagagctaagattatctggggaaatcaaaacaaaaa
                                                                                                                                                                            DB 10;
                                                                                                                                                                          Score 357.8; DB 10
Pred. No. 3.6e-36;
0; Mismatches 98
                                                                                                                                                                         7.0%;
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                                                                                                                                                                                              529; Conservative
                                                                                                                                                                                     Similarity
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                                                                                                                                   211
                                                                                                                                                                           Query Match
                                                                                                                                                                                     Best Local
Matches 52
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DEFINITION
                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                 516
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AA230070
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6

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Best Local Similarity
Matches 371; Conserv
                                                                                                                                                                            human.
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                                                AA659567/c
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //note="Vector: paMpl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDC-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissaue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Anchael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -41ml3 fwd. ET from Amersham

High quality sequence stop: 230.
                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 349)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGGAAAGTCAAGCCCATCTATTTCCACCACCCAGTGAAGCATTGGAAACCCTATTTCCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 347.4; DB 10; Length 349;
Pred. No. 8.9e-35;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1.349
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/db_xref="taxon:9606"
/clone="IMAGE:1011443"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%;
                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348;
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Best Local 8
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                                                                                    REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                            COMMENT
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/ac_stage="45 years old"
/dev_stage="45 years old"
/lab_host="DBILOB"
/lab_host="DBILOB"
/note="Vector: pAMPIO; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
bNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMPIO by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nil.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.,
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 379)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 CTGCACTACTCCTCTGCAGTGCCTTGGGGAATTTCCTCTATTGGTGTACAGTCTGTCATG 317
AA659567 379 bp mRNA EST 05-NOV-1997 nt63a03.sl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1203148 similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.3e-34;
0; Mismatches 5; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_"IMAGE:1203148"
/clone_lib="NoI_CGAP_Pr3"
/sex="Male"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primàtes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%;
98.1%;
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AA659567.1 GI:2595721
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9

Gaps

19;

Length 536; Indels 4827

4945

q δ g δy g δy

137

LOCUS

18

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

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AZ017963 498 bp DNA GSS 25-FEB-2000 RPCI-23-259K23.TV RPCI-23 Mus musculus genomic clone RPCI-23-259K23
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Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) 0ther GSSs: RPCI-23-259K23.TJ Coher.GSSs: RPCI-23-259K23.TJ Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                           4531 atggtgagcgtggactttccggaaatgatggcagagatcatctctgtgcaagtgcccaag 4590
                                                                                                                                                                                                                                                                                                                         4591 atcetttetgggaaagteaageeeatetattteeacaeeeeagtgaageattggaaaeeet 4650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4948 tgtcaagttgtgcttgtttacagcac--tactctgtgccagccacacaaacgtttactta 5005
                                                                                                                                                                                                                                                   4828 ttccctccctatctaaccctcccatggcaccttcagactttgcttcccattgtggctcct 4887
                                                                                                                               9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
                                        6.3%; Score 319; DB 10;
81.7%; Pred. No. 2.9e-31;
                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ017963.1 GI:7093347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
                                    Ouery Match
Best Local Similarity 81.77
Matches 446; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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LOCUS
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KEYWORDS
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 536)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Lacy,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
197 CCTATCTGTTTTGAATGGTGTTTGTATGCCTTTAAATCTGTGATGATCTCATATGGCC 138
                                                                                                                                                                                                                                                                                                 A1315085 536 bp mRNA EST 17-DEC-1998 uj23g04.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1920822 3' similar to gb:X53779 Mouse mRNA for androgen receptor (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1920822"
/clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 487.
Location/Qualifiers
1. .536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female"
                                                                                                                                                                           5065 aagcaaacaaaaaaaa 5082
                                                                                                                                                                                              AAGCAAACAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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AI315085/c
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USA

BASE COUNT

ORIGIN

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                                                                                                                                                                                                                                                                                                                                              /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
DcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
BCOR1 sites. The ligation products were transformed into
DHOB electrocompetent cells (BRL Life Technologies).

175 c 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
library availability, please contact Pieter de Jong (pieter@dejong.med.bufalo.edu). Clones may be purchased from BACPAC Resources (http://wacpac.med.buffalo.edu/orderingframe.htm). or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 259 row: K column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1985 acccagaggccgcgagcgcagcactcccggcgccagtttgctgctgctgcagcagcagc 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1865 tggaagtgcagttagggctgggaagggtctaccctcggccgccgtccaagacctaccgag 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GAGCGTTCCAGAATCTGTTCCAGAGCGTGCGCGAACCGATCCAGAACCCGGCCCCAGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AGCAGGCAGCCTCCGAGGCCACCTGAGAGCAGCTCCCCCGAGCCTGGGGCGCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2285 tggccgccagcaaggggctgccgcagcagctgccagcacctccggacgaggatgactcag
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Pred. No. 5.3e-28;
0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-259K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctgacettaaagacateetgagegagg 2431
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                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 73.9
Matches 419; Conservative
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                                                                                                                                                             Class: BAC ends.
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/dev_stage="45 years old"
/dev_stage="45 years old"
/lab_host="0H10B"
/note="wector: pAWPI0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAWPI0 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
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                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs_remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D., CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgtgcttgtttacagcactactctgtgccagccacacaaacgtttacttatcttatgcca 5015
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                                                                                                                                                                                                                                                           Primates; Catarrhini; Hominidae;
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Pred. No. 6.1e-27;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -28mils revl ET from Amersham
High quality sequence stop: 250.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1011443"
/clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.68;
                                                                                                                                      AA229714.1 GI:1851877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 292)
                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                Homo sapiens
                                                                nc49b06.rl similar to
                                                                                                                  AA229714
                                            AA229714
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                                                                                                                                                                                          human.
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ORIGIN
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RESULT 13
AA229714/C
                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                      REFERENCE
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KEYWORDS
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AI659563/C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
I (bases 1 to 395)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSS: RPCI-23-127M1.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 103 c 129 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong pieterédejong mad buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: Plate: 17x row. M column: 1
Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
/lab_host="PH10B"
/note="Yorgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Yorgan: Kidney/Female C57BL/6J mouse kidney and/or
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
                                                                                                                                AZ267276 395 bp DNA GSS 26-JUL-2000
RPCI-23-127M1.TJ RPCI-23 Mus musculus genomic clone RPCI-23-127M1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4470 cgigcagcciatigcgagagagcigcaicagilcacilligaccigciaalcaagicaca 4529
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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/clone="RPCI-23-127M1"
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                                                                                                                                                                                                           AZ267276.1 GI:9480889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhao@tigr.org
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                                                                                                                                                                       DNA sequence.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI659563 247 bp mRNA EST 10-MAY-1999 tul2d12.xl NCI_CGAP_Pr28 Homo sapiens CDNA clone IMAGE:2250839 3/ similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence. AI659563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 247)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                    4650 tatttccccaccccagctcatgcccctttcagatgtcttctgcctgt--tataactctg 4707
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100.0%; Pred. No. 6.1e-21;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:2250839"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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238; Conservative
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